

Figure 1 125P5C8 SSH sequence

GATCACGTGCTGTCGATATCCTTCACATTGCCATGTTCA
GAGCTGTAGATAATCTCTGGAGCCAGGTGCTGAAGTGA
TATATCCCAGAAATATCACTTGATTAGAGCTACTTTCA
GAGTTGAAACAGCAATAGCCTGCAGTTCTGTCGAG
GTCATCTCGTGGTCCCCAAAGTGTGTCACGACAAAATC
ACCAGCTGCCGAAATGTTAACGGTCAATGTGATGGCT
GGTGCAGCTTGCTGTGTTGCCAGGCTGGTCTAACGTGCAGA
TAGATC

Figure 2 Double stranded sequence and ORF for 125P5C8-Pro-pCR2.1.

1	M	T	S	L	W	R	E	I	L	L	E	S	L	L	G	C	V	S
ATG	ACC	TCG	CTG	TGG	AGA	GAA	ATC	CTC	TTG	GAG	TCG	CTG	CTG	GGA	TGT	TTT	TCT	
W	S	L	Y	H	D	L	G	P	M	I	Y	Y	F	P	L	Q	T	
TGG	TCT	CTC	TAC	CAT	GAC	CTG	GGA	CCG	ATG	ATC	TAT	TAC	TTT	CCT	TTG	CAA	ACA	
L	E	L	T	G	L	E	G	F	S	I	A	F	L	S	P	I	F	
CTA	GAA	CTC	ACT	GGG	CTT	GAA	GGT	TTT	AGT	ATA	GCA	TTT	CTT	TCT	CCA	ATA	TTC	
L	T	I	T	P	F	W	K	L	V	N	K	K	W	M	L	T	L	
CTA	ACA	ATT	ACT	CCT	TTC	TGG	AAA	TTG	GTT	AAC	AAG	AAG	TGG	ATG	CTA	ACC	CTG	
L	R	I	I	T	I	G	S	I	A	S	F	Q	A	P	N	A	K	
CTG	AGG	ATA	ATC	ACT	ATT	GGC	AGC	ATA	GCC	TCC	TTC	CAG	GCT	CCA	AAT	GCC	AAA	
L	R	L	M	V	L	A	L	G	V	S	S	S	L	I	V	Q	A	
CTT	CGA	CTG	ATG	GTT	CTT	GCG	CTT	GGG	GTG	TCT	TCC	TCA	CTG	ATA	GTG	CAA	GCT	
V	T	W	W	S	G	S	H	L	Q	R	Y	L	R	I	W	G	F	
GTG	ACT	TGG	TGG	TCG	GGA	AGT	CAT	TTG	CAA	AGG	TAC	CTC	AGA	ATT	TGG	GGA	TTC	
I	L	G	Q	I	V	L	V	V	L	R	I	W	Y	T	S	L	N	
ATT	TTA	GGA	CAG	ATT	GTT	CTT	GTT	CTA	CGC	ATA	TGG	TAT	ACT	TCA	CTA	AAC		
P	I	W	S	Y	Q	M	S	N	K	V	I	L	T	L	S	A	I	
CCA	ATC	TGG	AGT	TAT	CAG	ATG	TCC	AAC	AAA	GTG	ATA	CTG	ACA	TTA	AGT	GCC	ATA	
A	T	L	D	R	I	G	T	D	G	D	C	S	K	P	E	E	K	
GCC	ACA	CTT	GAT	CGT	ATT	GGC	ACA	GAT	GGT	GAC	TGC	AGT	AAA	CCT	GAA	GAA	AAG	
K	T	G	E	V	A	T	G	M	A	S	R	P	N	W	L	L	A	
AAG	ACT	GGT	GAG	GTA	GCC	ACG	GGG	ATG	GCC	TCT	AGA	CCC	AAC	TGG	CTG	CTG	GCA	
G	A	A	F	G	S	L	V	F	L	T	H	W	V	F	G	E	V	
GGG	GCT	GCT	TTT	GGT	AGC	CTT	GTG	TTC	CTC	ACC	CAC	TGG	GTT	TTT	GGA	GAA	GTC	
S	L	V	S	R	W	A	V	S	G	H	P	H	P	G	P	D	P	
649	TCT	CTT	GTT	TCC	AGA	TGG	GCA	GTG	AGT	GGG	CAT	CCA	CAT	CCA	GGG	CCA	GAT	CCT
N	P	F	G	G	A	V	L	L	C	L	A	S	G	L	M	L	P	
703	AAC	CCA	TTT	GGA	GGT	GCA	GTA	CTG	CTG	TGC	TTG	GCA	AGT	GGA	TTG	ATG	CTT	CCA
S	C	L	W	F	R	G	T	G	L	I	W	W	V	T	G	T	A	
757	TCT	TGT	TTG	TGG	TTT	CGT	GGT	ACT	GGT	TTG	ATC	TGG	TGG	GTT	ACA	GGA	ACA	GCT
S	A	A	G	L	L	Y	L	H	T	W	A	A	A	V	S	G	C	
811	TCA	GCT	GCG	GGG	CTC	CTT	TAC	CTG	CAC	ACA	TGG	GCA	GCT	GCT	GTG	TCT	GGC	TGT
V	F	A	I	F	T	A	S	M	W	P	Q	T	L	G	H	L	I	
865	GTC	TTC	GCC	ATC	TTT	ACT	GCA	TCC	ATG	TGG	CCC	CAA	ACA	CTT	GGA	CAC	CTT	ATT
N	S	G	T	N	P	G	K	T	M	T	I	A	M	I	F	Y	L	
919	AAC	TCA	GGG	ACA	AAC	CCT	GGG	AAA	ACC	ATG	ACC	ATT	GCC	ATG	ATA	TTT	TAT	CTT
L	E	I	F	F	C	A	W	C	T	A	F	K	F	V	P	G	G	
973	CTA	GAA	ATA	TTT	TTC	TGT	GCC	TGG	TGC	ACA	GCT	TTT	AAG	TTT	GTC	CCA	GGA	GGT
V	Y	A	R	E	R	S	D	V	L	L	G	T	M	M	L	I	I	
1027	GTC	TAC	GCT	AGA	GAA	AGA	TCA	GAT	GTG	CTT	TTG	GGG	ACA	ATG	ATG	TTA	ATT	ATC
G	L	N	M	L	F	G	P	K	K	N	L	D	L	L	L	Q	T	
1081	GGG	CTG	AAT	ATG	CTA	TTT	GGT	CCT	AAG	AAA	AAC	CTT	GAC	TTG	CTT	CAA	ACA	
K	N	S	S	K	V	L	F	R	K	S	E	K	Y	M	K	L	F	
1135	AAA	AAC	AGT	TCT	AAA	GTG	CTT	TTC	AGA	AAG	AGT	GAA	AAA	TAC	ATG	AAA	CTT	TTT
L	W	L	L	V	G	V	G	L	L	G	L	G	L	R	H	K	A	
1189	CTG	TGG	CTG	CTT	GTT	GGT	GTG	GGA	TTG	TTG	GGA	TTA	GGA	CTA	CGG	CAT	AAA	GCC
Y	E	R	K	L	G	K	V	A	P	T	K	E	V	S	A	A	I	
1243	TAT	GAG	AGA	AAA	CTG	GGC	AAA	GTG	GCA	CCA	ACC	AAA	GAG	GTC	TCT	GCT	GCC	ATC
W	P	F	R	F	G	Y	D	N	E	G	W	S	S	L	E	R	S	
1297	TGG	CCT	TTC	AGG	TTT	GGA	TAT	GAC	AAT	GAA	GGG	TGG	TCT	AGT	CTA	GAA	AGA	TCA
A	H	L	L	N	E	T	G	A	D	F	I	T	I	L	E	S	D	
1351	GCT	CAC	CTG	CTC	AAT	GAA	ACA	GGT	GCA	GAT	TTC	ATA	ACA	ATT	TTG	GAG	AGT	GAT
A	S	K	P	Y	M	G	N	N	D	L	T	M	W	L	G	E	K	
1405	GCT	TCT	AAG	CCC	TAT	ATG	GGG	AAC	AAT	GAC	TTA	ACC	ATG	TGG	CTA	GGG	GAA	AAG
L	G	F	Y	T	D	F	G	P	S	T	R	Y	H	T	W	G	I	
1459	TTG	GGT	TTC	TAT	ACA	GAC	TTT	GGT	CCA	AGC	ACA	AGG	TAT	CAC	ACT	TGG	GGG	ATT
M	A	L	S	R	Y	P	I	V	K	S	E	H	H	L	L	P	S	
1513	ATG	GCT	TTG	TCA	AGA	TAC	CCA	ATT	GTG	AAA	TCT	GAG	CAT	CAC	CTT	CCG	TCA	
P	E	G	E	I	A	P	A	I	T	L	T	V	N	I	S	G	K	
1567	CCA	GAG	GGC	GAG	ATC	GCA	CCA	GCC	ATC	ACA	TTG	ACC	GTT	AAC	ATT	TCG	GGC	AAG
L	V	D	F	V	V	T	H	F	G	N	H	E	D	D	L	D	R	

Figure 2 Cont'd

1621 CTG GTG GAT TTT GTC GTG ACA CAC TTT GGG AAC CAC GAA GAT GAC CTC GAC AGG
K L Q A I A V S K L L K S S S N Q V
1675 AAA CTG CAG GCT ATT GCT GTT TCA AAA CTA CTG AAA AGT AGC TCT AAT CAA GTG
I F L G Y I T S A P G S R D Y L Q L
1729 ATA TTT CTG GGA TAT ATC ACT TCA GCA CCT GGC TCC AGA GAT TAT CTA CAG CTC
T E H G N V K D I D S T D H D R W C
1783 ACT GAA CAT GGC AAT GTG AAG GAT ATC GAC AGC ACT GAT CAT GAC AGA TGG TGT
E Y I M Y R G L I R L G Y A R I S H
1837 GAA TAC ATT ATG TAT CGA GGG CTG ATC AGG TTG GGT TAT GCA AGA ATC TCC CAT
A E L S D S E I Q M A K F R I P D D
1891 GCT GAA CTG AGT GAT TCA GAA ATT CAG ATG GCA AAA TTT AGG ATC CCT GAT GAC
P T N Y R D N Q K V V I D H R E V S
1945 CCC ACT AAT TAT AGA GAC AAC CAG AAA GTG GTC ATA GAC CAC AGA GAA GTT TCT
E K I H F N P R F G S Y K E G H N Y
1999 GAG AAA ATT CAT TTT AAT CCC AGA TTT GGA TCC TAC AAA GAA GGA CAC AAT TAT
E N N H H F H M N T P K Y F L *
2053 GAA AAC AAC CAT CAT TTT CAT ATG AAT ACT CCC AAA TAC TTT TTA TGA AAC

Figure 3 Amino acid sequence of 125P5C8.

1 MTSLWREILL ESLLGCVWS LYHDLGPMIY YFPLQTLELT GLEGFSIAFL 50
51 SPIFLTITPF WKLVNKKWML TLLRIITIGS IASFQAPNAK LRLMVLALGV 100
101 SSSLIVQAVT WWSGSHLQRY LRIWGFI LGQ IVLVVLR IWY TSLNPIWSYQ 150
151 MSNKVILTLS AIATLDRIGT DGDCSKPEEK KTGEVATGMA SRPNWLLAGA 200
201 AFGSLVFLTH WVFGEVSLVS RWA VSGH PHP GPDPNPFGGA VLLCLASGLM 250
251 LPSCLWFRGT GLIWWVTGTA SAAGLLYLHT WAAA VSGCVF AIFTASMWPQ 300
301 TLGHЛИNSGT NPGKTMTIAM IFYLLEIFFC AWCTAFKFVP GGVYARERSD 350
351 VLLGTMMLII GLNMLFGPKK NLDLLLQTKN SSKVLFRKSE KYMKLFLWLL 400
401 VGVGLLGLGL RH KAYERKLG KVAPTKEVSA AIWPFRFGYD NEGWSLERS 450
451 AHLLNETGAD FITILES DAS KP YMGNNDLT MWLGEKLGFY TDFGPSTRYH 500
501 TWGIMALSRY PIVKSEHHLL PSPEGEIAPA ITLTVNISGK LVDFVVTHFG 550
551 NHEDDLDRKL QAI AVSKLLK SSSNQVIFLG YITSAPGSRD YLQLTEHGNV 600
601 KDIDSTDHDR WCEYIMYRGL IRLGYARISH AELSDSEIQM AKFRI PDDPT 650
651 NYRDNQKVVI DHREVSEKIH FNPRFGSYKE GHNYENNHHF HMNTPKYFL 699

Figure 4A Alignment with AK025164 protein product

Score = 1397 bits (3615), Expect = 0.0
Identities = 682/699 (97%), Positives = 683/699 (97%)

Query: 1 MTSLWREILLESLLGCVWSLYHDLGPMIYYFPLQTLELTGLEGSIAFLSPIFLTITPF 60
MTSLWREILLESLLGCVWSLYHDLGPMIYYFPLQTLELTGLEGSIAFLSPIFLTITPF
Sbjct: 1 MTSLWREILLESLLGCVWSLYHDLGPMIYYFPLQTLELTGLEGSIAFLSPIFLTITPF 60

Query: 61 WKLVKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY 120
WKLVKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY
Sbjct: 61 WKLVKKWMLTLLRIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQRY 120

Query: 121 LRIWGFIGQIVLVVLRIWYTSLNPIWSYQMSNKVILTLSAIATLDRIGTDGDCSKPEEK 180
LRIWGFIGQIVLVVLRIWYTSLNPIWSYQMSNKVILTLSAIATLDRIGTDGDCSKPEEK
Sbjct: 121 LRIWGFIGQIVLVVLRIWYTSLNPIWSYQMSNKVILTLSAIATLDRIGTDGDCSKPEEK 180

Query: 181 KTGEVATGMASRPNWLLAGAAGFSLVFLTHWVFGESLVSRAVSGHPHPGPDPNPFGGA 240
KTGEVATGMASRPNWLLAGAAGFSLVFLTHWVFGESLVSRAVSGHPHPGPDPNPFGGA
Sbjct: 181 KTGEVATGMASRPNWLLAGAAGFSLVFLTHWVFGESLVSRAVSGHPHPGPDPNPFGGA 240

Query: 241 VLLCLASGLMLPSCLWFRGTGLIWWVTGTASAAGLLYLHTWAAAASGCVFAIFTASMWPQ 300
VLLCLASGLMLPSCLWFRGTGLIWWVTGTASAAGLLYLHTWAAAASGCVFAIFTASMWPQ
Sbjct: 241 VLLCLASGLMLPSCLWFRGTGLIWWVTGTASAAGLLYLHTWAAAASGCVFAIFTASMWPQ 300

Query: 301 TLGHLINSGTNPGKMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLGTMMLII 360
TLGHLINSGTNPGKMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLGTMMLII
Sbjct: 301 TLGHLINSGTNPGKMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLGTMMLII 360

Query: 361 GLNMLFGPKKNLDLLQTKNSSKVLFRKSEKYMXXXXXXXXXXXXXRHKAYERKLG 420
GLNMLFGPKKNLDLLQTKNSSKVLFRKSEKYMK RHKAYERKLG
Sbjct: 361 GLNMLFGPKKNLDLLQTKNSSKVLFRKSEKYMKFLWLLVGVGLLGLRHKAYERKLG 420

Query: 421 KVAPTKEVSAAIWPFRFGYDNEGWLRSERAHLLNETGADFITILESDASKPYMGNDLT 480
KVAPTKEVSAAIWPFRFGYDNEGWLRSERAHLLNETGADFITILESDASKPYMGNDLT
Sbjct: 421 KVAPTKEVSAAIWPFRFGYDNEGWLRSERAHLLNETGADFITILESDASKPYMGNDLT 480

Query: 481 MWLGEKLGFYTDGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLTVNISGK 540
MWLGEKLGFYTDGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLTVNISGK
Sbjct: 481 MWLGEKLGFYTDGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLTVNISGK 540

Query: 541 LVDFVVTHFGNHEDDLRKIQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNV 600
LVDFVVTHFGNHEDDLRKIQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNV
Sbjct: 541 LVDFVVTHFGNHEDDLRKIQAIAVSKLLKSSSNQVIFLGYITSAPGSRDYLQLTEHGNV 600

Query: 601 KDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRIPIPDDPTNYRDNQKVVI 660
KDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRIPIPDDPTNYRDNQKVVI
Sbjct: 601 KDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRIPIPDDPTNYRDNQKVVI 660

Query: 661 DHREVSEKIHFNPRTFSYKEGHNYENNHHFHMNTPKYFL 699
DHREVSEKIHFNPRTFSYKEGHNYENN+FHMMNTPKYFL
Sbjct: 661 DHREVSEKIHFNPRTFSYKEGHNYENNHFHMNTPKYFL 699

Figure 4B Alignment with yeast YCR017 cp Protein

Score = 261 bits (668), Expect = 1e-68
Identities = 204/705 (28%), Positives = 330/705 (45%), Gaps = 50/705 (7%)

Query: 15 GCVWSWSLYHDLGPMIYYFPLQTLELTGLEGSIAFLSPIFLTTPFWKLVNKWMLTLLR 74
G + WS L I++FPL + ++G E + +L PIFL + PF ++ + L
Sbjct: 279 GFLFWSNVTSLLCSIWHFPLWYMGISGYEAAILGYLGPIFLYL-PFVSEAFHQYGVLLGG 337

Query: 75 IIITIGSIASFQAPNAKLRLMVLALGVSSSLIVQAVTWWSGSHLQ-RYLRIWGFIKGQIVL 133
II IG+ Q P +L + + ++ + VQ + + + + + W +LG +
Sbjct: 338 IIIAIGAYI-VQMPELRLISVAVGTSITVATFVQNLRYITNAETSFSFALTW--LLGLVAS 394

Query: 134 VVLRIWYTSLNPIWSYQMS-----NKVILTLSAIATLDRIGTDGDCSKPEEKKTGEVATG 188
V+L++ + + NP W NK L L+ + + + + E K+ + +
Sbjct: 395 VILKMGFYTNNPTWVILDERNGGYNKTALVLTFLFGM--LSPYVNSINFEGKRNAQAKS- 451

Query: 189 MASRPNWLLAGAAFGLSVFLTHWVFGEVSLVSRWAVSGHPHP-GPDPNPFGGAVLCLAS 247
AS L FGSL+F H + + S WA G+ GP P P+G L C
Sbjct: 452 -ASLIGKLFALVGFGSLLFGIHQLLTDSTTIYWAEGYNESHGPLPWPWGA--LTCTVM 508

Query: 248 GLMLPSCLWFRGTGLIWWVTGTASAAGLLY--LHTWAAAV-SGCVFAIFTASMWPQ---T 301
S + F G L+ + S A L + W + G ++AI + P
Sbjct: 509 LFASLSSVKFMGKPLVPCLLLLSTAVLSARSITQWPKYIFGGLLYAIAMLWLVP SYFSA 568

Query: 302 LGHLINSGTNPGBTMTIAMIFYLLEIFFCAWCTAFKFVPGGVYARERSDVLLGTMMIIG 361
LG + N ++ Y++ + W A+ FVP G RE+ + +L I
Sbjct: 569 LGQVQNIWV----YVLSFSVVIIFVLAHVWVVAYAFVPMGWVLREKIETVLAFSSTFII 623

Query: 362 LNMLFGPKKNLDLLQTKNSSKVLFRKSEKYMXXXXXXXXXXXXXXRHKAYERKLGK 421
+ L N+ L+ K +F R R G
Sbjct: 624 IGALTCKNLNIQLVTMGKKFFIYVF-----FFAVALLSLTARFVYDIRPTGI 670

Query: 422 VAP----TKEVSAAIWPFRFGYDNEGSSLERSAHLNETGADFITILESDASKPYMGNN 477
P ++ ++A IW FG DN+ W+S +R +L+ + D + +LE+D + MGN
Sbjct: 671 PQPYHPDSQLITAGIWTIHFLDNDMWASEDRMINLIKDMELDVGLLETDTQRITMGNR 730

Query: 478 DLTMWLGEKLGFYTDGPSTRYHTWGIMALSRYPIVKSEHHLLPSPEGEIAPAITLT-N 536
DLT L L Y DFGP HTWG + LS++PIV S HHLLPSP GE+APAI T+
Sbjct: 731 DLTSKLAHDLNMYADFGPGPNKHTWGCVLLSKFPIVNSTHLLPSPVGELAPAIHATLQT 790

Query: 537 ISGKLVDVFVTHFGNHEDDLDRKLQIAIVSKLLKSSSNQVIFLGYITSAPGSRDY-LQLT 595
+ LVD V H G ED+ DR+LQ+ ++KL+ +++ I L Y+ PG +Y ++
Sbjct: 791 YNDTLVDVFVHFSGQEEDEEDRRLQSNYMAKLMGNTTRPAILLSYLVVDPGEGNYNTYVS 850

Query: 596 EHGNVKDIDSTDHDRWCEYIMYRGLIRLGYARISHAELSDSEIQMAKFRIPIPDDPTNYRDN 655
E + DID +D DRWCEYI+YRGL R GYAR++ ++D+E+Q+ KF++ + ++
Sbjct: 851 ETSGMHDIDPSDDDRWCEYIYLGYRGLRTGYARVARGTITDTELQVGKFQVLSEQA-LVEH 909

Query: 656 QKVVIDHREVSEKIHFNPRFGSYKEGHNYENNHFHM-NTPKYFL 699
+ ++ +SE + + +F G E H +H+ + P+Y+L
Sbjct: 910 SDSMYEYGHMSEPEYEDMKFPDKFLGEG-ERGHFYHVFDEPRYYL 953

Figure 5

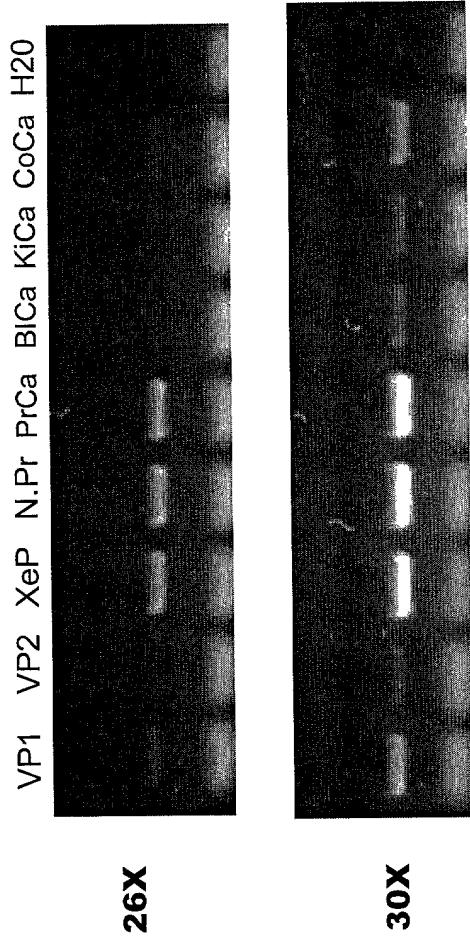


Figure 6A

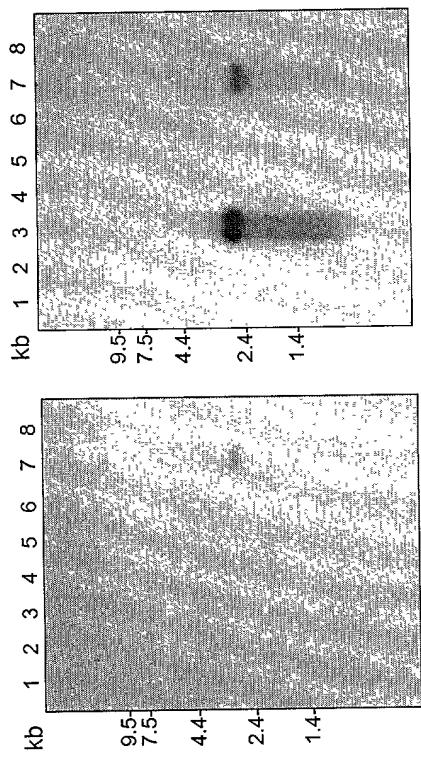


Figure 6B

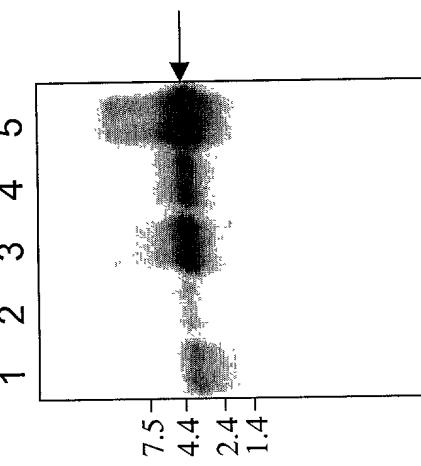


Figure 6C

Figure 7

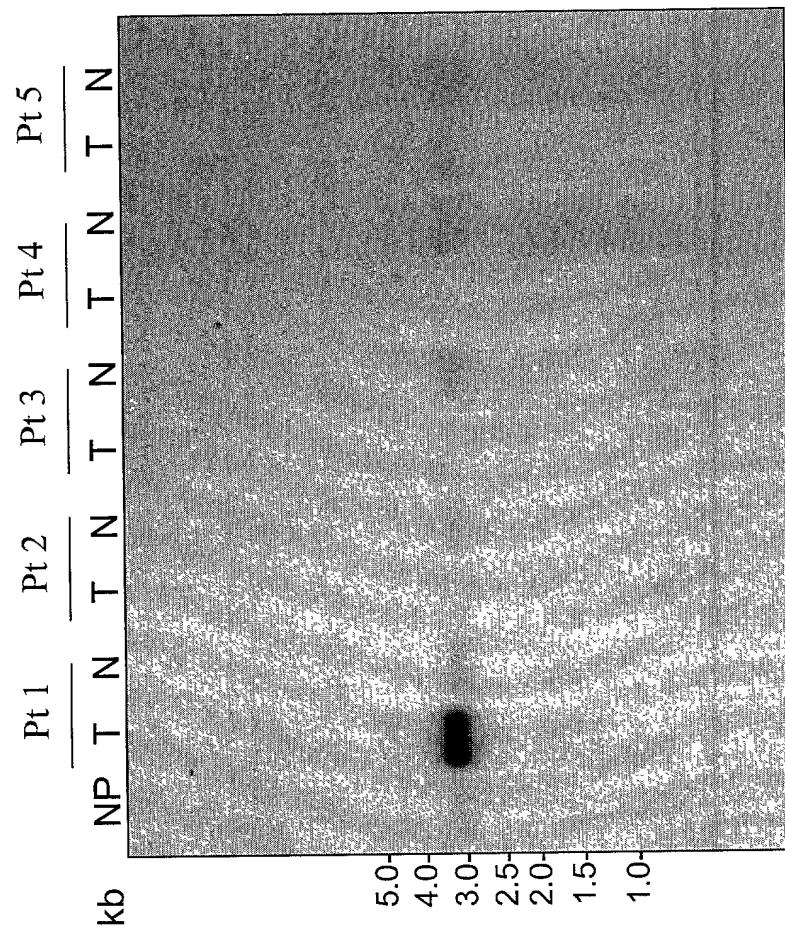


Figure 8

